

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:01:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354863.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR22354863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354863_1.fastq.gz SRR22354863_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:01:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354863.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	177,280,132
Mapped reads	174,249,832 / 98.29%
Unmapped reads	3,030,300 / 1.71%
Mapped paired reads	174,249,832 / 98.29%
Mapped reads, first in pair	87,256,215 / 49.22%
Mapped reads, second in pair	86,993,617 / 49.07%
Mapped reads, both in pair	173,837,182 / 98.06%
Mapped reads, singletons	412,650 / 0.23%
Secondary alignments	0
Supplementary alignments	7,210,071 / 4.07%
Read min/max/mean length	30 / 150 / 151.47
Duplicated reads (estimated)	160,699,846 / 90.65%
Duplication rate	86.29%
Clipped reads	104,677,193 / 59.05%

2.2. ACGT Content

Number/percentage of A's	5,763,295,653 / 27.5%
Number/percentage of C's	4,521,870,740 / 21.58%
Number/percentage of T's	5,876,661,908 / 28.05%
Number/percentage of G's	4,791,505,896 / 22.87%
Number/percentage of N's	451,060 / 0%

GC Percentage	44.45%
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2.3. Coverage

Mean	6.7715
Standard Deviation	368.5341

2.4. Mapping Quality

Mean Mapping Quality	53.69
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2.5. Insert size

Mean	469,745.06
Standard Deviation	7,968,018.19
P25/Median/P75	92 / 140 / 211

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	121,501,744
Insertions	3,149,715
Mapped reads with at least one insertion	1.71%
Deletions	3,437,799
Mapped reads with at least one deletion	1.9%
Homopolymer indels	43.69%

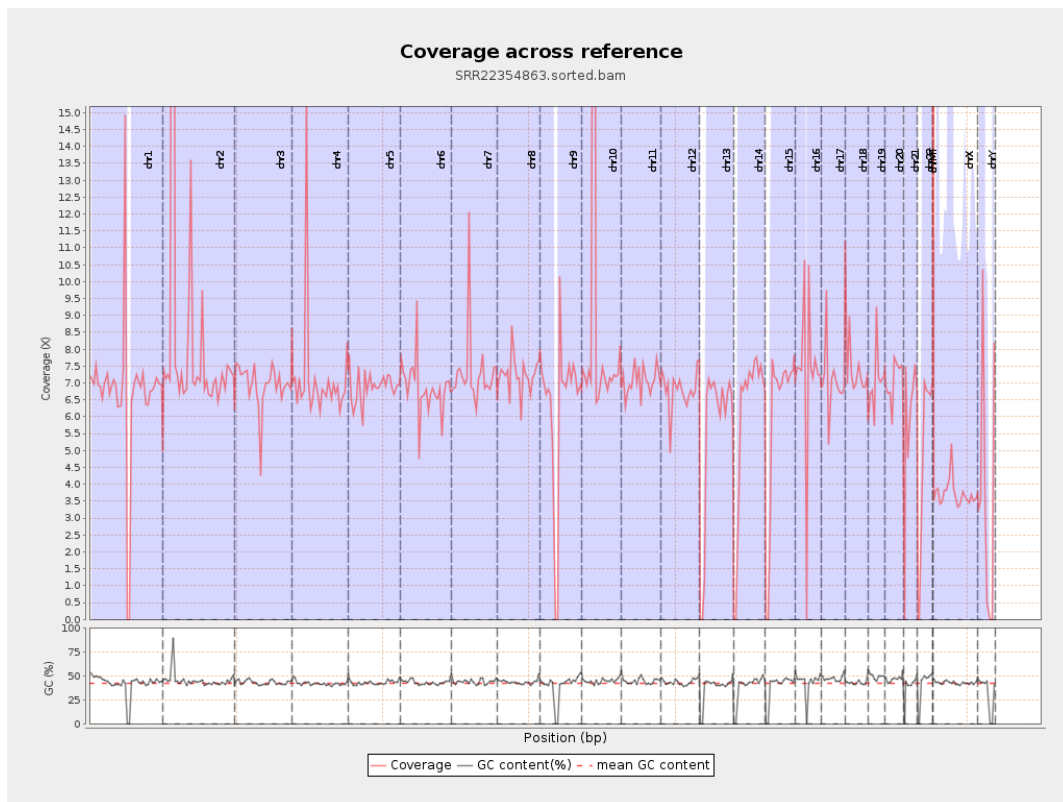
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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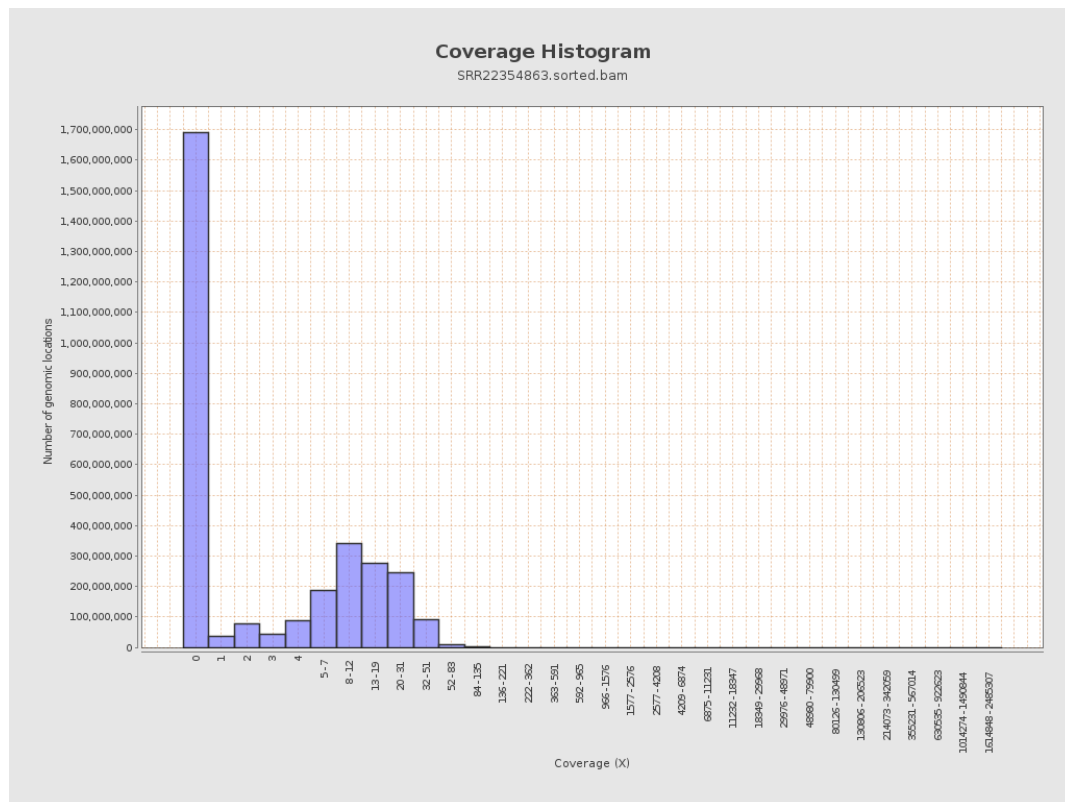
		bases	coverage	deviation
chr1	249250621	1671190297	6.7049	177.4447
chr2	243199373	2051184210	8.4342	1,282.6124
chr3	198022430	1376732831	6.9524	18.3312
chr4	191154276	1362550305	7.128	62.4117
chr5	180915260	1246701174	6.8911	11.3724
chr6	171115067	1170050032	6.8378	29.0163
chr7	159138663	1162500590	7.305	132.4305
chr8	146364022	1057386166	7.2244	24.4816
chr9	141213431	894260399	6.3327	81.4748
chr10	135534747	1146276435	8.4574	195.5774
chr11	135006516	951063935	7.0446	35.6613
chr12	133851895	910091406	6.7992	11.3608
chr13	115169878	639903616	5.5562	9.5734
chr14	107349540	650774362	6.0622	50.9934
chr15	102531392	602858405	5.8797	9.8953
chr16	90354753	657059778	7.272	38.0864
chr17	81195210	574859841	7.08	39.1525
chr18	78077248	580985537	7.4412	81.4597
chr19	59128983	417447388	7.0599	87.6008
chr20	63025520	444794510	7.0574	23.6574
chr21	48129895	288887704	6.0023	40.4254
chr22	51304566	245960619	4.7941	23.306
chrMT	16571	57315263	3,458.7691	672.8557
chrX	155270560	579827047	3.7343	16.5607

chrY	59373566	221805246	3.7358	84.7944
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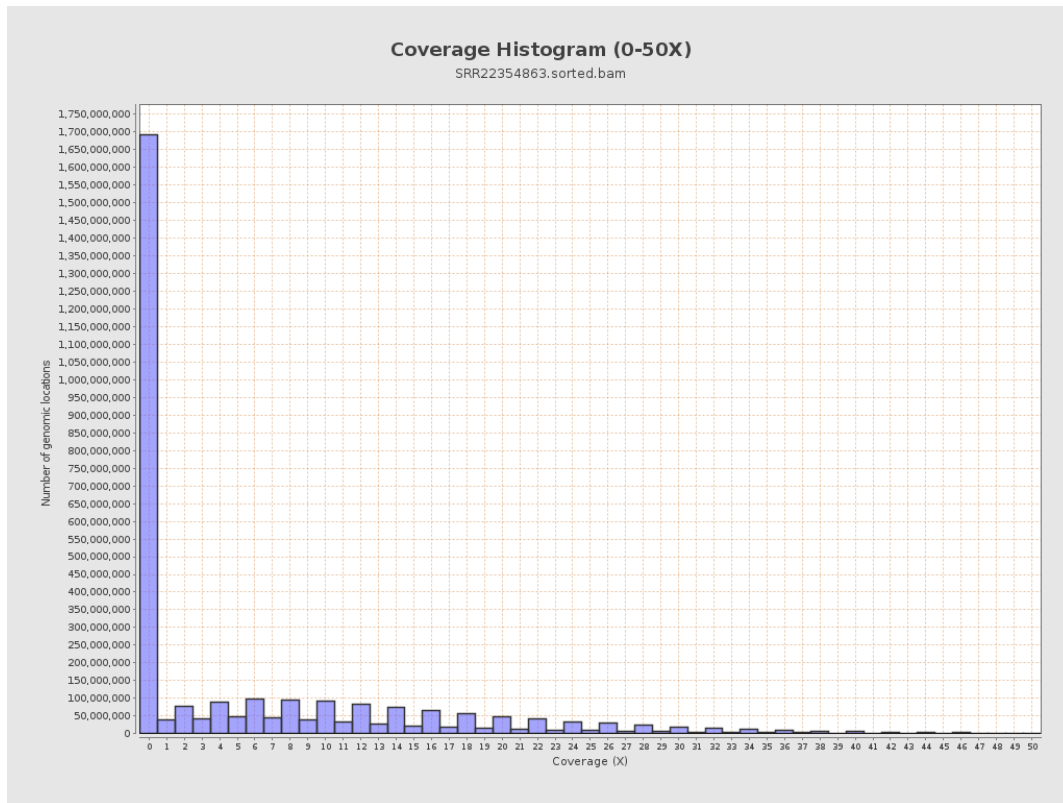
3. Results : Coverage across reference



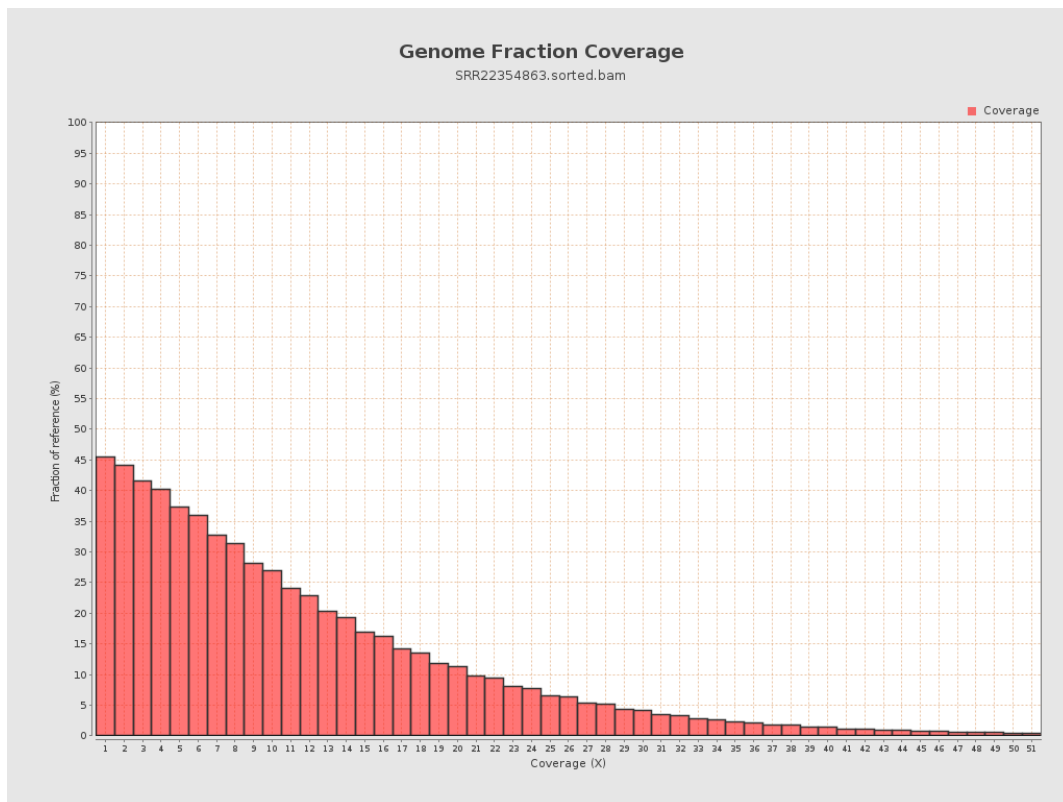
4. Results : Coverage Histogram



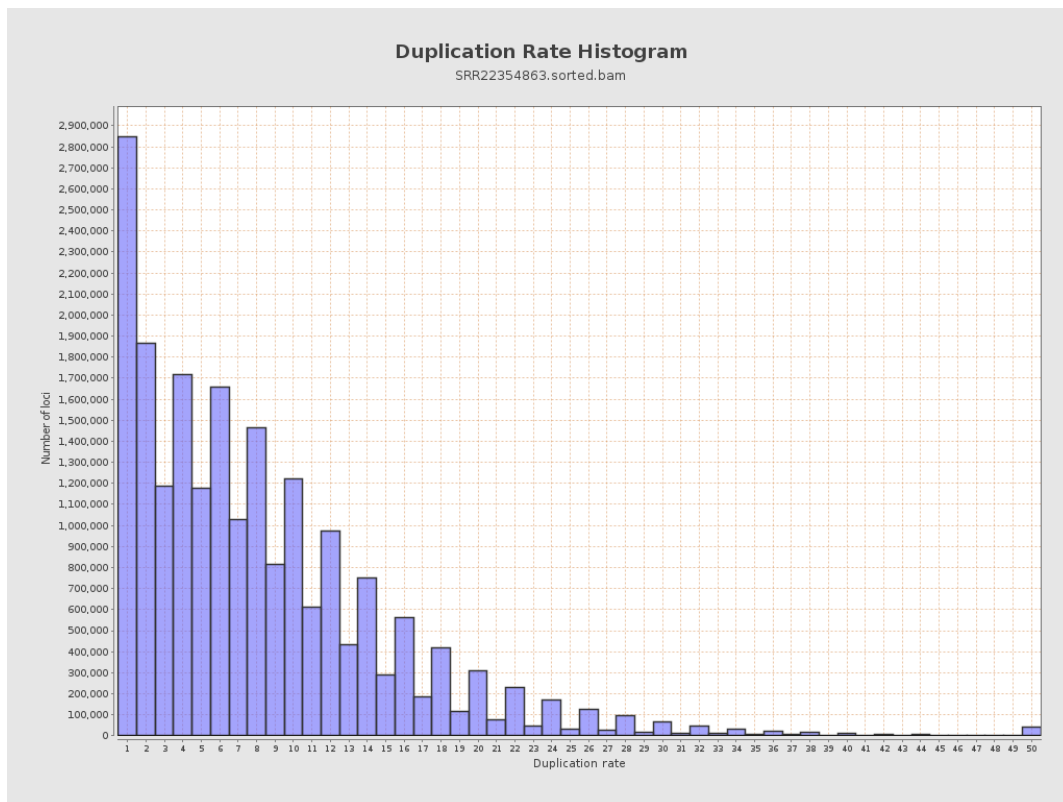
5. Results : Coverage Histogram (0-50X)



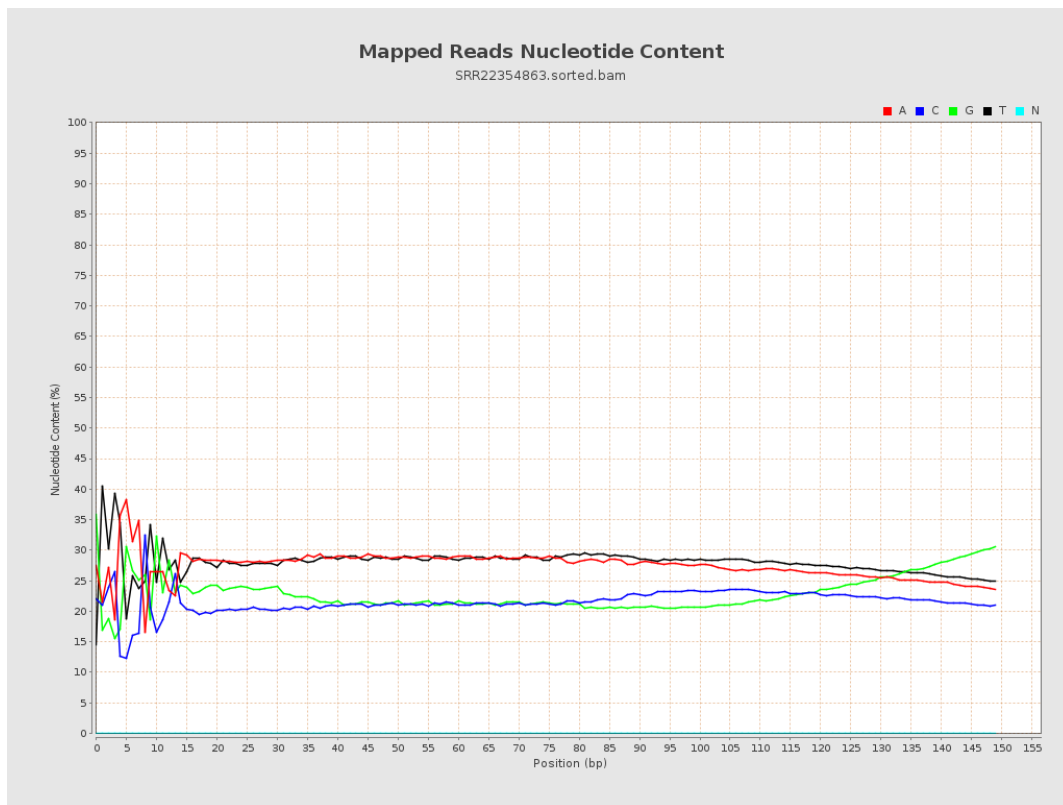
6. Results : Genome Fraction Coverage



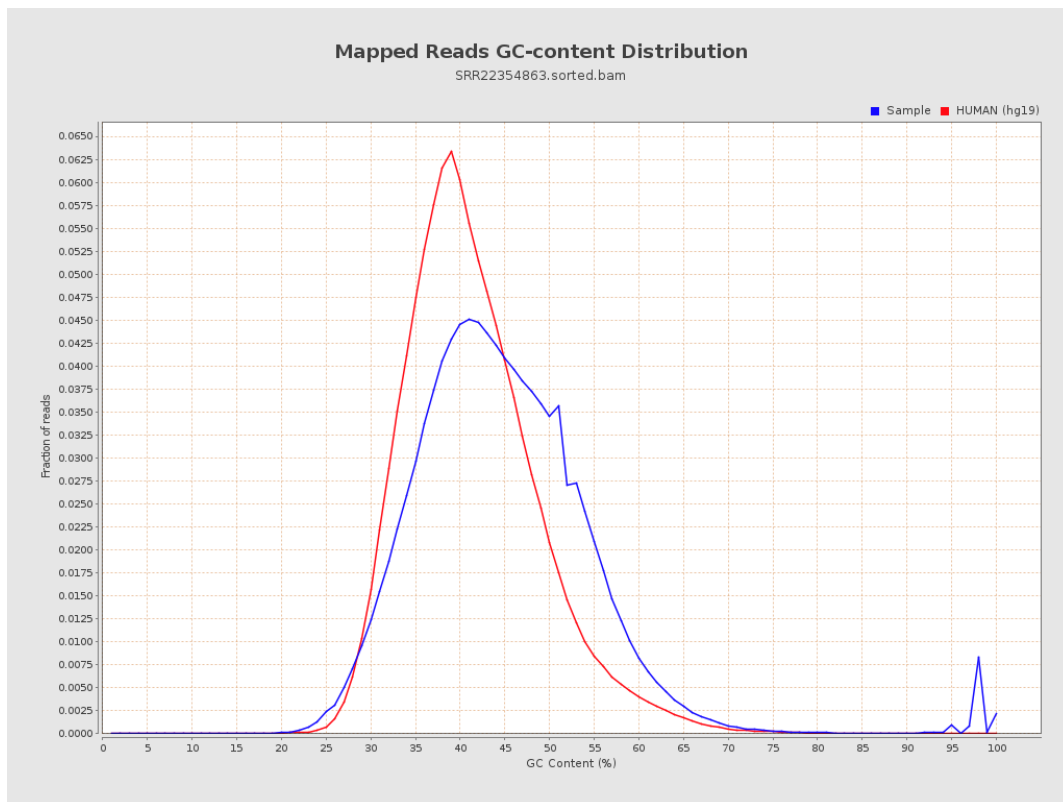
7. Results : Duplication Rate Histogram



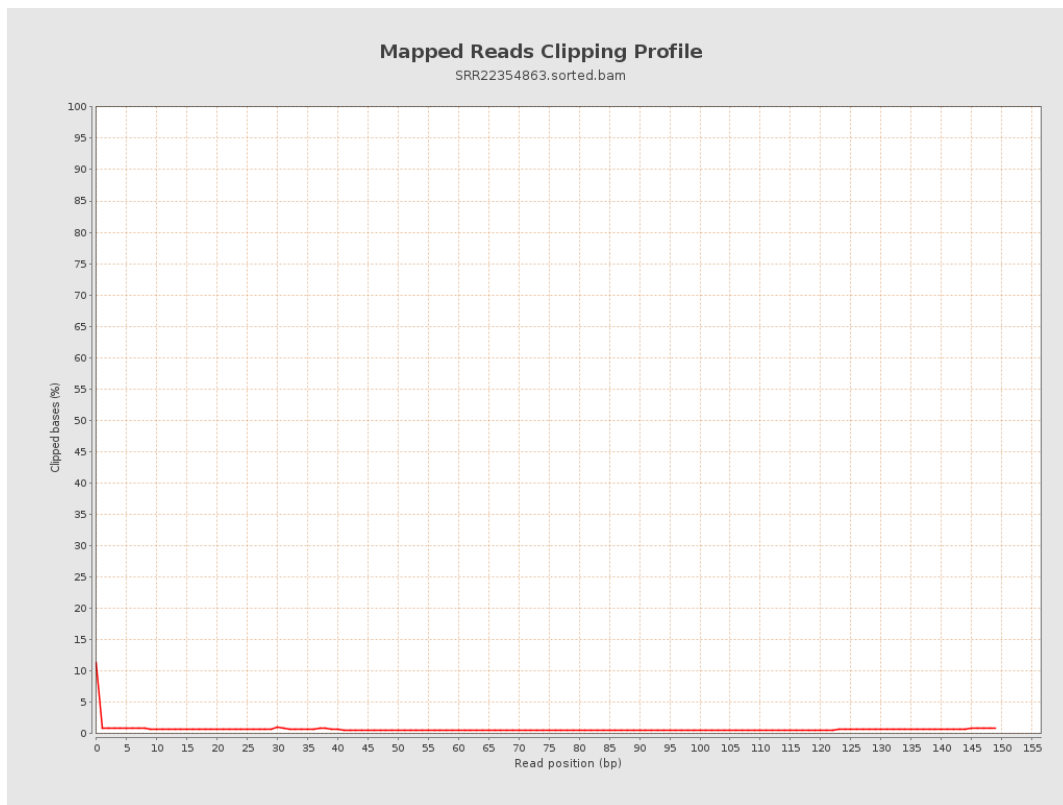
8. Results : Mapped Reads Nucleotide Content



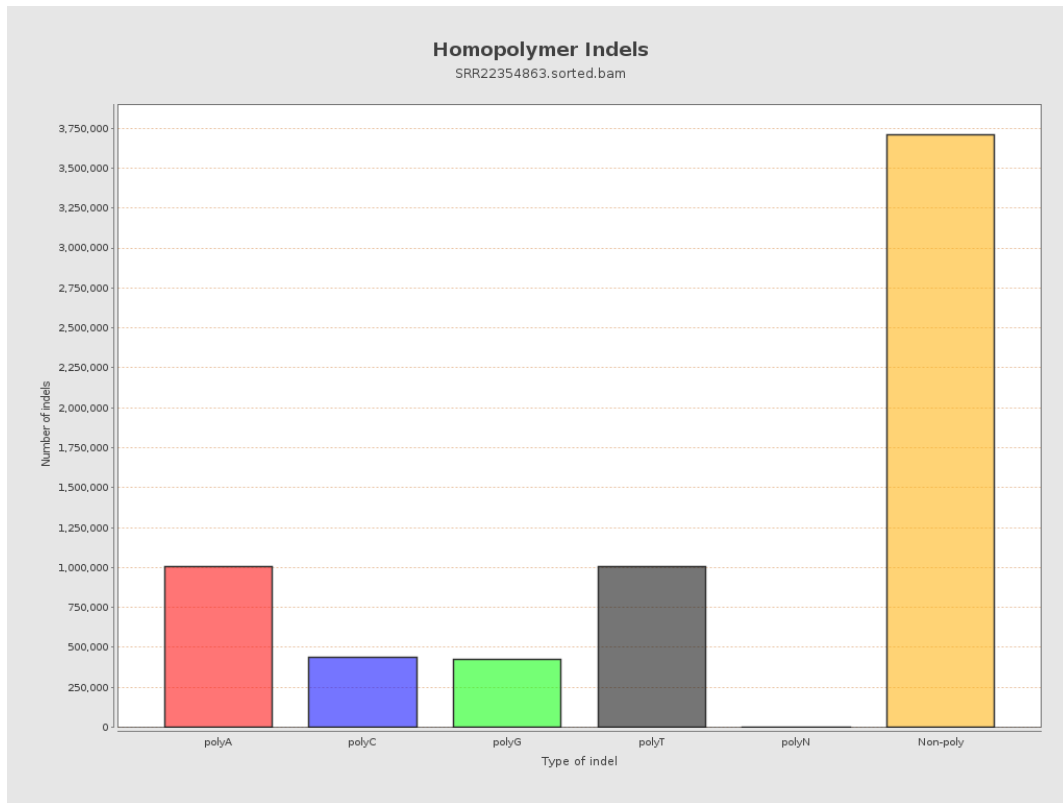
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



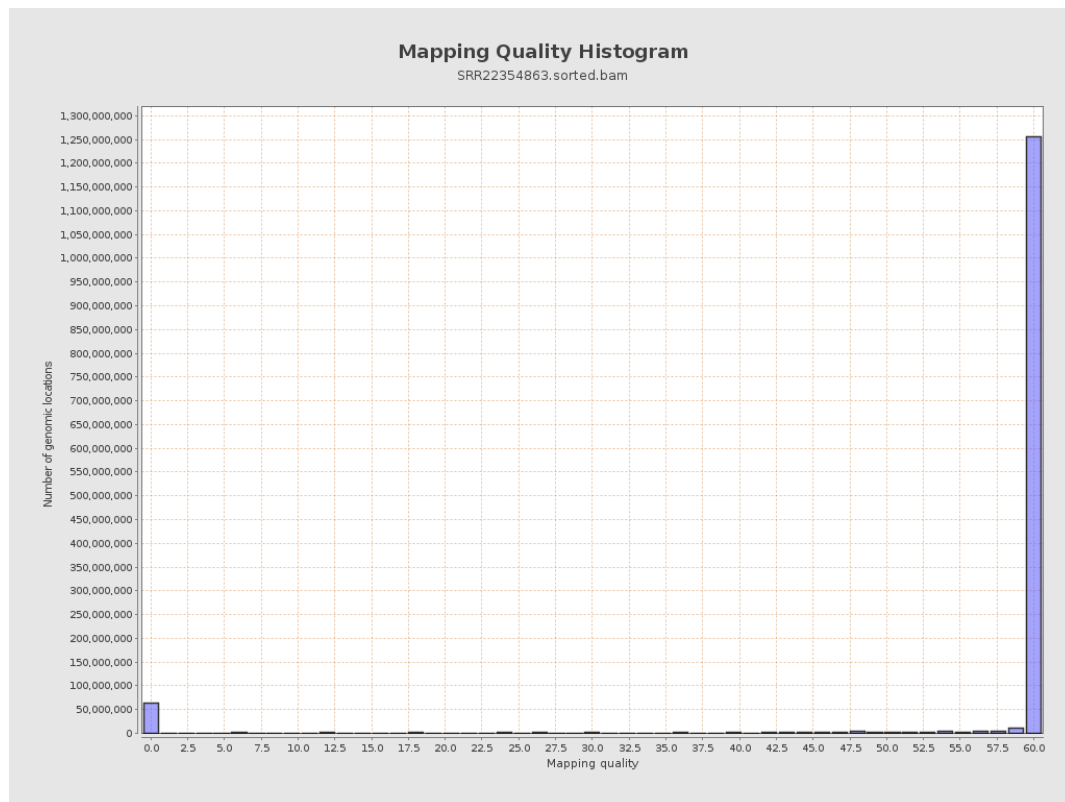
11. Results : Homopolymer Indels



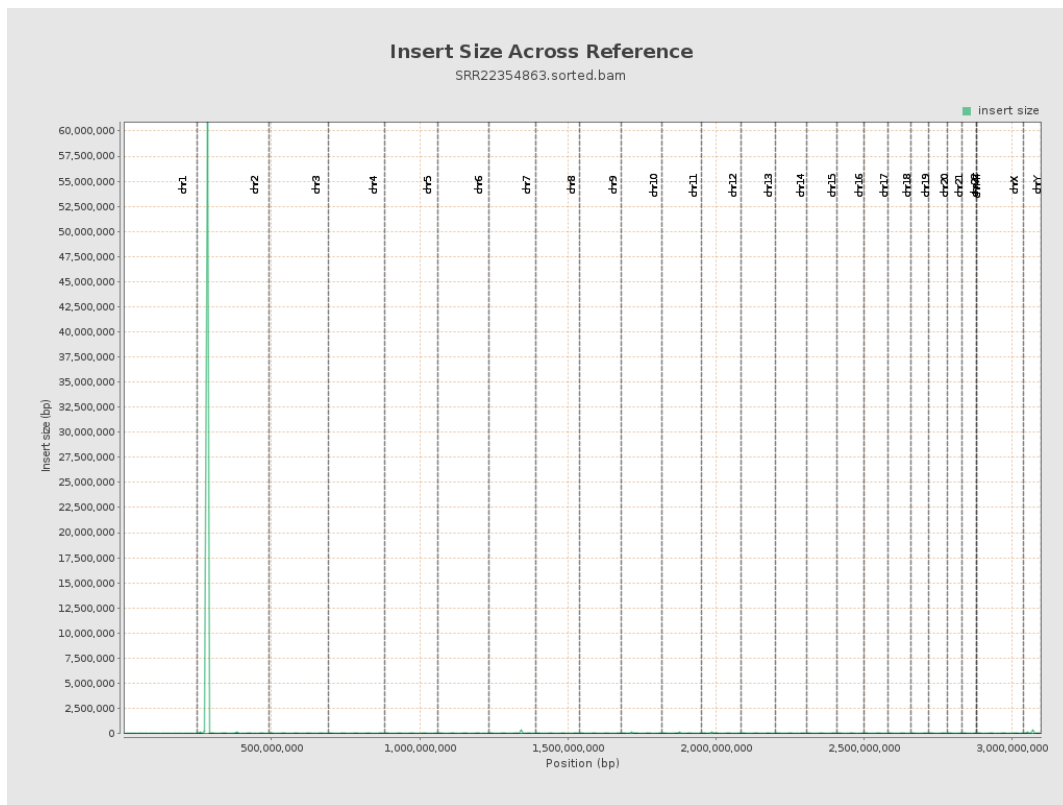
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

